

LENGTH: 3625 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Query Match 57.5%; Score 942.6; DB 10; length 3625;
 Best Local Similarity 74.2%; Pred. No. 1.5e-220; Matches 1191; Conservative 0; Mismatches 415; Indels 0; Gaps 0;

QY 1 ATGGCAAAAGAACATCAATTTCAGAGATGCGGTCTGCAGGGACTTAT 60
 Db 364 ATGGCAAAAGAACATCAATTTCAGAGATGCGGTCTGCAGGGACTTAT 423

QY 61 ATGTTAGAGATACCTCAAGAACCTTGCTCTAAGGGCGATGTGTCCTGA 120
 Db 424 GTATTAGAGATACAGTGAAGAGTACATTGGCGCTAAAGTCTAACGTTAGAA 483

QY 121 AAAGTTTGTCTCCCTTAATTAATCTAATAGGAGGGTACCTGTAAGAGATCGA 180
 Db 484 AACATATTTGGTCACCATGATCTACATAGGATGAGTACAAATGCTAAGGAAATTGAA 543

QY 181 TTAGAGAGATTTGAAACAGTGGCAATTGGTGTGAGGAGCTCTAAACC 240
 Db 544 TTGGAGAGATCTTTGAAACATGGCGCAAAATTAGTCAGAGTGTCTTAACAG 603

QY 241 ATGATATTCGGTGTGATGGAGGACTACTGACACAGTTTGACACGGCTAT 300
 Db 604 ATGATATTCGGTGTGACGGACACAGCAGCTGTTGACACGGCTATGTCG 663

QY 301 GAGGACTAAAMAATGACGCGCTTGAAAGGCTTGACATGGTATCCATGTCGAGGATGAA 360
 Db 664 GRAGGCTTAAACACTAACTGCTGGAGCAACCCGTTAGGTATCTCGTGGGATTGAA 723

QY 361 ACAGCAACAGCACAGCAGCTGTTGACAGCAGCTGTTGACACGGCTAT 420
 Db 724 TTGAGAACAAACAGCAGCTGTTGACAGGATGACATGTTGATGTCGAA 783

QY 421 GAGCTTATGCGCAGTCGCTCGAGTATCATCGCTGCTGTTGAGGATAT 480
 Db 784 GAACGATGTCGACAGTGCCTGTTGAGGATGACGCGCTTAATGAAAGGG 903

QY 541 ATGGAACAGACAGCTGAGTGGTGAAGGATGCCATTGACGGTGTACTCTCA 600
 Db 904 ATTAAACAGATTTAGTGGTGTGAGGAATGCAATTGCGGTTATTATCCAA 963

QY 601 TACATGGCAGAGCATGAAATGGTGTGAGCTTGAAACCGATTATCTTAA 660
 Db 964 TACATGGTACTGACACGATAAATGGAGGTGTTTGGAAATCTCATATCTTAA 1023

QY 661 ACGGATTAAGAACGTCACACCTCCAGAACATTCCACTACTTGAGGATCTAA 720
 Db 1024 ACCGACACAAACATCTCAATATTCAGATACTTACCTTTATGACAAATCTCAAA 1083

QY 721 ACCGACCGTCATACATCATGCGAGTAGTGTGAGGCGAACACTCAACCTT 780
 Db 1084 CARAGCCCTCCACCTGATGTTGGAGTGTGAGGAACTTACACACTTA 1143

QY 781 GTCTTGACAAAGATTCGTTGAGCTTGCTCAAGCGCAGGATGGT 840
 Db 1144 GTATTGACAAATCCGGGGRACATTAAATGTTGCGCAAAAGCGCCAGGATGGT 1203

QY 841 GATCGTGTAAAGTCTGACAGACATGCTATCTTACAGTGTGAGTGTAC 900
 Db 1204 GACCGCCGCAAGGAGTGTGAGATTTACAGGCTGACTAACT 1263

QY 901 GAGGATCTAGCTGTGAAATGAGTGTGAGATTTACAGGCTGACTAACT 960

Db 1264 GACCACTTASGGTTAGACTTAAGAACACAACTATGAAATGCTAGCAA 1323

QY 961 ATTACAGTGATAAGATAGGACAGTAAATGTTGAGGTCAGGAGTCAGATT 1020
 Db 1324 GTATGTCGCAAAAGATACACACAAATGTCGAGGAGCTGTTCAAAAGGCCATT 1383

QY 1021 GCTTACCGTATGACTGATAAAGCAATAGAACACAACTCTGACTTGACCGT 1080
 Db 1384 GATCCCGCGCTTCAATTAAACCAATTGGCGAACACGGCTGTGTTGAGCT 1443

QY 1081 GAAAACTACAGAGAGCTTGCGGAATAGSTGTTGGGTGTTACTCTTAACTAAGTGGAA 1140
 Db 1444 GAAAACTACAGAGAGCTTGCGTAATTTAGTGTGTGGGTTCTGTTAAGGCGT 1503

QY 1141 GTCGACACAGAGACTTAAAGAAATGAAACTTGCTGAGGATGTTAAGGCT 1200
 Db 1504 GCTGCAACTGACAGAATTAAGAATTTACAGATTTAGTGTGTGGGTTCTGTTAAGGCGA 1563

QY 1201 ACACGTCACCGGTGAGGANGGTTCTGCTGTTGGAGCAGACTTACCGT 1260
 Db 1564 ACACGTCACCGGTGAGGANGGTTCTGCTGTTGGGTTCTGTTAAGGCGA 1623

QY 1261 ATGAAAAAGTAGCAGCTCTGAGCTGAGGCGATGATGCTACTGGAGTACATGTC 120
 Db 1624 ATGGTAAAGTCGCTGCGCTGAAGCTGAGGTCAGGTCACAGGGTCAGATGTC 1183

QY 1321 CTGCGCTCTAGAGGCGCTGAGCTGCAATTGTTAAATGCGGGTACGGAGCTCC 1380

Db 1684 GTCGCGCTAGAGAACCCATCGTCGAAATCTCGTGAAGAAATCTGTTGAGGATCA 1743

QY 1381 GTAGTGTATGACAGTGTGAAACAGGCCCTCGCAGACAGGATTTACCTGCAACAGGT 1440

Db 1744 GCGATGTTGCAAACTAAAMAATGTCGTTGACTTGTAGTCATGTCACGCTAACGGT 1803

QY 1441 GATGGCTTATGATTAACAGGAACTATGACCTGAGGCTGAAGTACACGATAGCG 1500
 Db 1804 GATGGTAAACAGTGTGAGGCGGTATTGACCCACAAAGTACTGCTGTC 1663

QY 1501 CTGAAATGCACTTAAAMAATGTCGTTGACTTGTAGTCATGTCACGCTAACGGT 1660

Db 1864 TTACAAATGCTGTTGTCAGCTGTTTAAACAGGATGACAGGACTTGTAA 1823

QY 1561 AAACCTGACCACTGCGAGCCAGCAGTGCAGGAGTATGG 1606

Db 1924 AAACGAGAACGCTGCAACGCTCTATGATGGTCATCATCATGAG 1969

RESULT 3
 US-09-790-988-1
 Sequence 1, Application US/09790988
 Patent No. US0020121687A1
 GENERAL INFORMATION:
 APPLICANT: SHIGENOBU, SHUJI
 APPLICANT: WATANAE, HIDEKI
 APPLICANT: HATTORI, MASAHIRA
 APPLICANT: SAKAKI, YOSHIOUKI
 TITLE OF INVENTION: GENOME DNA OF BACTERIAL Symbiont OF APHIDS
 FILE REFERENCE: 081356-0159
 CURRENT APPLICATION NUMBER: US/09-790-988
 CURRENT FILING DATE: 2001-02-23
 PRIOR APPLICATION NUMBER: JP2000-107160
 PRIORITY FILING DATE: 2000-04-07
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 640681
 TYPE: DNA
 ORGANISM: Buchnera sp.
 US-09-790-988-1

Query Match 37.6%; Score 615.8; DB 10; length 640681;
 Best Local Similarity 62.8%; Pred. No. 2.1e-139; Matches 991; Conservative 0; Mismatches 582; Indels 6; Gaps 2;

QY 4 GCAAAAGAATCAATTTCAGCAGATGCCGTGCGCATGTCGCTGCGCGAGTGATG 63
 Db 18721 GCTAAAGATCTAAATTGGAAAGCAGCCGCAATTAAATCTCTGGAGTTATGTA 18780
 QY 64 TTACAGATACCGTCAAAGTAACTACGCTGTTGGCTTAAGGGCGCAATTGTCGAA 123
 Db 18781 TTACGATACCGTCAAAGTAACTACGCTGTTGGCTTAAGGGCGCAATTGTCGAA 18840
 QY 124 GCTTGGTCTCCPAAATCTATGACCGGGTAACTATGCTTAAGAGATCGATTA 183
 Db 18841 TCTTGGACCCCTAGTATGATCTAATGATGTTGACCGCGTAAATGTA 18900
 QY 184 GAGATCATTTAACACAGGGCAAATGCGTCTGAGTGTGCTCTAACAT 243
 Db 18901 GAGATAATTGCAACATGGAGCTCAAATGTAAGAAGGAGPAAATGATGTTA 18960
 QY 244 GATATGCTGCTGATGGAGGAGACTGCAACAGTTGACACAGCCATGTC 303
 Db 18951 GATGCGAGCAGGAGTGTGACCAACAGCACAATTAAGACAT 19020
 QY 304 GGCATTAACATGACGGGGCTAACTCAATTGCTATCGGTCGAGCATGAA 363
 Db 19021 GGTAAAGCAGTACAGCTGATGCTGATGCTGAACTGTTGATGAA 19080
 QY 364 GCAAGCACACGCTGTGAGCTGATGCTGAAACCCATTGCTCAACCTG 423
 Db 19081 GCTGTTATGACTCTGAGAGATTAAACATTATCTGACCATGTC 19140
 QY 424 GCTATGCGCAGCTGCTGAGCATCATCAGCC--TGAAGTGGAGATATC 480
 Db 19141 GCAATTACAGTGTGACTATATCTGCAACATCAGTGAAGAAGTGTGTTAAT 19200
 QY 481 TCAGAGCTATGAGGGTGGGCAAGATGTTGATTAACATGAGAATCTGG 540
 Db 19201 GCGAGGAGCATGAGTAAAGTGTGAACTGAGGAGTTATGAGGATG 19260
 QY 541 ATGAAACAGACTTGAGGGTGAAGGATGCAATTGACGGGTACTGTC 600
 Db 19261 TTACAGGGAGACTGTAAGTGCAGAACGGTGAATTGCTGGTATCTC 19320
 QY 601 TACATGGTCACAGCATGAAATGGTCACACCTGAAACCCATTCTTATC 660
 Db 19321 TATTTCATCAATTAACACAGATGCTGAAACCCATTCTTATC 19380
 QY 661 AGGATAAAAGTGTCAACACATCCAAGACATTGCCACTTGAGAATTAA 720
 Db 19381 GCTGTATAAAATAACTATGTTGCGAAATGTTGCAAA 19440
 QY 721 ACCAACCGCTCCATTACTCATTTGAGATGTTGAGTGTGATGTTGAGCTCCAACTT 780
 Db 19441 TCAGGAAACCCCTTAATTAATCTGAGATGAGGTTGAGCTTAACTT 19500
 QY 781 GCTCTGACAGATCGGGTACTTCAGTGTGCTGCAAGGCCGAGTTG 840
 Db 19501 CTGTTTAATCTGAGGAGATGTTAAGTGCAGCAGTAAGCAGCTGATG 19560
 QY 841 GATCCTGCTAAAGCTATGTTGAGCATGCTCTGAGGTGGACAGTGTAC 900
 Db 19561 GATGCTCTAAAGCAATGTTACAGATTCATCTTCTACTGTTCTCT 19620
 QY 901 GAGGATCTGAGCTGATTAAGATGTCACATGACGCCCTGGACGCTCTAAG 960
 Db 19621 GAGATCTGAGCTGATGAAATCTGTTGACAGTGTGAGCTGAACT 19680
 QY 961 ATTACAGTGTAAAGATGACAGCTAATGTTGAGGTTGAGCTGAGCTT 1020
 Db 19681 GTTATTATGACAGACTACAACTATPATGTTGTTGAGGAAACACCT 19740
 QY 1021 GCTTACCTATGCACTGTTAATGCAATTGACACAACTCTGACTTGCCTG 1080
 Db 19741 CAAGCTGTTATGCAATTGCCACAGAAATTCAAGAAGTACTCTGATGAA 19800
 QY 1081 GAAACTCTAGAGAAGCTTGGCAATTACTGTTGTTGAGCTTAAGTAGGA 1140
 Db 19801 GAAATTAATGAACTGCTTACGCTTACGCTGAAATGCGGGCTGTTAAGCTG 1180
 QY 1141 GTCCTACAGAGACCTTAAAGAAATGAACTTGTGCTGAGCTTAATGCT 1200
 Db 19861 GCGCTTACAGAGTAAATGTTGCTGAGGAGCTTAATGCT 19920
 QY 1201 ACAGCGCGCGCTTAAAGAGATGTTGCTGAGCTTATTAGCT 1260
 Db 19921 ACTCTGCGAGCTGAGAGTGTGAGTGTGAGTGTGAGGTTGCTG 19980
 QY 1261 ATTGAAAGTAGCAGCTGCTGAGCTGAGGAGTATGCTACTGGCTA 1317
 Db 19981 GCGGGAAATGCTTACCTGGCTAAATGAGTAAAGACGTTGAGCT 20040
 QY 1318 GPGCTTGGCTACTAGAGCTGAGCTGAGCTCAATTGTTAATGCTGGTAAAGGGC 1377
 Db 20041 GCTTGGGCGATGAGCTCATTAGCTCAATTGCTTAATCTGGTAAAGAACCT 20100
 QY 1378 TCCGTTATGAGAGTGAACACGCCGAGACAGATTATGCTGCAACA 1437
 Db 20101 TCTGTTATCAGATGTTAAAGAGGCTTACATGTTGTTACAGCT 20160
 QY 1438 GGTGAGTGGTGTGATGTTAAACAGGAGATGACCTGTCAGACGAC 1497
 Db 20161 GATGATATGCGAGATGTTGTTGTTGTTTATGTCACACTTAATGTTACGGCT 20220
 QY 1498 GGCCTTAAATGAGCTCTGAGTGTGAGCTTATGACAGAGGAGTGTGCT 1557
 Db 20221 GCTTTCAGTGTGCTGCTGCTGCTGCTGCTTAATGTCACAGATGTTACGGCT 20280
 QY 1558 ATAAACCTGACCCCTA 1576
 Db 20281 GACTTGCCTAAAGAAGATA 20299
 RESULT 4
 US-09-960-428-13
 ; Sequence 13, Application US/09/960428
 ; General Information
 ; Patent No. US20020115147A1
 ; APPLICANT: Roche Diagnostics GmbH
 ; TITLE OF INVENTION: Method for producing an active heterodimeric AMV-RT in prokary
 ; FILE REFERENCE: 5272/00/
 ; CURRENT APPLICATION NUMBER: US/09/960,428
 ; CURRENT FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 13
 ; LENGTH: 2155
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli
 ; US-09-960-428-13
 QY 36.0% Score 589.8; DB 10; Length 2155;
 Best Local Similarity 61.3%; Pred. No. 2.4e-134; Matches 986; Conservative 0; Mismatches 617; Indels 6; Gaps 2;
 Db 478 GCTAAAGCTTAAATGGTACGCCCTGGCTGCAATTGCGGGCTGTTAAGCTG 537
 QY 64 TTACAGATACCGTCAAAGTACGCTGTTGCTTAAGGGCGCAATTGTTCTGTTAAGCTG 123
 Db 538 CTGCGAGCTGAGCTGAAAGTACCTCGTGGCTCAAAGGCCGTTACCTGTTCTGTTAAGCTG 597
 QY 124 GCTTGGTCTCCCTTAATCTAATGACGCCCTGGCTGCAATTGCGGGCTGTTAAGCTG 183
 Db 598 TCTTCTGCTGACGCCCTACCAAGATGTTGTTCTGCTGTTGCTGTTAATGCTG 657
 QY 184 GAGATCATTTGAAAGATGGGCAAAATGGTGTGAGTGTGCTCTAACAC 243

Db	658	GAAGACAACTTCGAAATATGGGCGCCAGNTGGTGAAGAAGAATGCGCTCTAAAGCAAC	717	Oy	1318	GTGCTTGCTGTCTAGAGAGGCTGTACTCCAAATGCTTAATGCTGGTACGAGGC	1377
Oy	244	GATATGCTGGTATGGGAGACTACTGCAACACTTGTGACAGCACAGCTTCATGAA	303	Db	1798	GCATGGTGTGCAATGAGCTCGGCTGCGTCAGTCATGACTCGGGGAGARCC	1857
Db	718	GACGCTGCAGGGACGACATCACACGCACTGACCCATACGGCTACATCATGAA	777	Oy	1378	TCCGTGTTATGACAACTGAAACAGGATCTGCACTGCTGCAATGCTGAGGCA	1437
Oy	304	GEACTAAAGAATGACAGCAGGAGCTGCTAACTCCAAATGGTATCGCTGAGGCA	363	Db	1858	TCTGTGTTGCTAACGGTAAAGCCTGAGGCTAACGCTAACGTTACAGCAGCACC	1917
Db	778	GGCTCAAAAGCTTCTGGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA	837	Oy	1438	GGTAGGGGTGATGATGATGAAACAGGATCTGACCCCTGAGGCTAACGATCA	1497
Oy	364	GAACACGCAACGCTTGTGAGCTGAAAGCCATTGTCACACTGCACTGCACTGAA	303	Db	1918	GRACAAATGGCAGACATGTCACATGGTACATGGTACATGGTACATGGTAC	1977
Db	838	GGGGTACCGCTCAGITGAGGACTGAGCTGAGGAGGAGGAGGAGGAGGAGGAA	897	Oy	1498	GGCTTAAATGAGCTCTGCTACTCTGCTATTTGCAACAGAGGAGGAGGAGGAG	1557
Oy	424	GTTATGCTCAGCTCTGCACTGAGGATCTGAGCTACGGCTACCGAGGAGGAGGAA	480	Db	1978	GCTCTGAGTACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2037
Db	898	GGCAGTGCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA	957	Oy	1558	AATAACTGACGAGCTACGCCACGCCAGGAGCTACGCCAGGAGTGGTAC	1605
Oy	481	TCAGAGCTATGGGGGGGCGACAGGATGTTGTTGATCACATGAGAAGATCTGAG	540	Db	2038	GACCTGCGAAACGATGCCAGCTGACTTGGGCTGCTGGTATGG	2086
Db	958	GCTGAGGCGATGACAACTGCGTTAAGAAGGGTTACCGGTGAGACGGTACCGT	1017				
Oy	541	ATGGAACAGACAGTGGTGAAGGATTTGACCGGGTACTCTGTC	600				
Db	1018	CTGCGAGGAGGAGACTGACGCGTGGTGAAGGATCTGCTGCT	1077				
Oy	601	TACARGGTCACACAGACATGAAACACGACATGGCAGACCTGAAACCAATTAACTTC	660				
Db	1078	TACTACATCAACAGCGGAACATGGCGCAGTAACTGGAAACCCATTACCTGGT	1137				
Oy	661	ACGGATAAAAGTGTGACACACCCAGACATTGCACTACTTGAGGAGTCTAA	720				
Db	1138	GTTGCAAAAGAAATCCTCACACCCGAGATGGTGTGCGGTCTGGAGCTGTTCCAA	1197				
Oy	721	ACCAACCCGCTCTACTCTTATGAGGAGTGTGATGGTGAACCTTACCC	780				
Db	1198	CGAGCAAACCCCTGCTGATCATGCTGAGATGAGGAGCTGAGCTGAGCAGCTG	1257				
Oy	781	GTCTGAGAAGATCTGGTACTTCATGATGTTGTTCTGCAAAAGGCCAGATTGT	840				
Db	1258	GTTGTTAACACCATGCGGCGACGCGAGTGGTAAAGACCGGGTTCGGC	1317				
Oy	841	GATCGCTGTAAGCTATGCTGAGACATGCTACTGCTGAGGTGGTACCTGATTCA	900				
Db	1318	GATCGCTGTAAGCTATGCTGAGGTGGTACCTGCTGAGGTGGTACCTGATTCT	1377				
Oy	901	GAGGATCPAGGCTGAATTAAGATGCTACATGACACCCCTGGAGGCTCTAG	960				
Db	1378	GRAGAGATGGATGGAGGAAAGAACACCCCTGGAGGACAGCCTGGTACAGCT	1437				
Oy	961	ATTACAGTGTGATGAGATGAGCAAGTAATGTTGAGGTTCAGAACTGATT	1020				
Db	1438	GTGTTGATCACAGAACACCCACTATCATGGATGGCTGGTGGAGAGCTGCA	1497				
Oy	1021	GCTTACACCTATGCTGACTGTTAAATGCTGACATTGAAACACACTTGTGACGT	1080				
Db	1498	CAGGGCGCTGTTGTCAGTCAGTCAGAGTGGAGGAGCTGAGCTGAGCGT	1557				
Oy	1081	GRAAACTACAGAAGAAGTGTGGCAATATGCTGTTGAGTGTGTTGAGTGA	1140				
Db	1558	GAAAACTGCGAGAACGGGTAGCGAACACGGGGCTTGCAGTAACTGGT	1617				
Oy	1141	GCTCCACAGACAGACGCTTAAAGAATGAGAACTTGTGAGGAGCTCTAACT	1200				
Db	1618	GCTGCTACCGAGGTTGAGATGAGAAAGACCGCTTAAAGCTGCGCAGCG	1677				
Oy	1201	ACAGGTGAGGCGTGTGGAGGACGACGACTATACGGT	1260				
Db	1678	ACCGGTTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA	1737				
Oy	1261	ATTGAAAGATGAGCAGCTGCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAA	1317				
Db	1738	CGCTCTAACTGCTGACCTGGCTGAGAACGAGAACGAGACGGGTACAAAGT	1797				
Oy	364	GCACACGAAACGCTGTTGAGCCATTGCTCACCTGCTCACCTGCTGCAAGGAA	423				

RESULT 5

US-09-841-132-380

Sequence 380, Application US/09841132

; Patent No. US2002006148A1

; GENERAL INFORMATION:

; APPLICANT: Bhatri, Avery A. W.

; APPLICANT: Siekly, Yasir A. W.

; APPLICANT: Probst, Peter

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

; FILE REFERENCE: 210121-46948

; CURRENT APPLICATION NUMBER: US/09/841,132

; CURRENT FILING DATE: 2001-04-23

; NUMBER OF SEQ ID NOS: 599

; SOFTWARE: FastSEQ for Windows Version 3.0/4.0

; SEQ ID NO: 380

; LENGTH: 1635

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

; US-09-841-132-380

; Query Match: 32.4%; Score: 530; DB: 10; Length: 1635;

; Best Local Similarity: 59.5%; Pred. No.: 7e-10; Mismatches: 636; Indels: 15; Gaps: 3;

; Matches: 957; Conservative: 0; Mismatches: 636; Indels: 15; Gaps: 3;

; DB: 7 GCGAAATTAAATTAATGAGGAGCCAGAAAATACAAAGGGTAAACT

; Oy: 4 GCAACGAACTCAATTTCTGAGATGCTGCGCTGCGAGTTGATG 63

; Db: 7 GCGAAATTAAATTAATGAGGAGCCAGAAAATACAAAGGGTAAACT

; Oy: 64 TTGAGGATACCGTCAAAGTACCGTCTGGTCTAAAGGCCAAUTGTGTTGAA 123

; Db: 67 CTGGAGGAGGAGTAAAGTGTACTCTGTTCTAAAGGAGCTCACCTGTTAAGTA 126

; Oy: 124 GCTTGGTCTCCCTATTAATCTGAGGAGCCAGGAACTTGTGCTGAGGATG 183

; Db: 127 AGCTTGCTCCCTGAGGAGTAAAGTGTGTTGAGTGTGTTGAGTAAAGT 186

; Oy: 184 GAGATCATTGAAACATGGGCAAAATGGGCTGAGTGGCTCTAAACCA 243

; Db: 187 GAGATACATGAAACATGGGCTGAGTGGAAAGTGGAGTGGCTCTAAACCA 246

; Oy: 244 GATATGCTGGTGTGAGGAGACTACTGCAACAGCTTGTGACAACTG 303

; Db: 247 GACAAAGCAGGCGGAGGAGTAACTGAGGAGTGTGTTGAGTAAAGT 306

; Oy: 304 GGCTAAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363

; Db: 307 GCTCTGAGAATTCACCTGCGGCTTACCTGAGGAGGAGGAGGAGGAG 366

; Oy: 364 GCACACGAAACGCTGTTGAGCCATTGCTCACCTGCTCACCTG 423

Db 367 CCCGTTAAAGTTGTTGATGACTCAAAAAATTAGTAAACCTGTRACACATCACAA 426
 Qy 424 GCTATGCTCAGGTCGTCGCACTATCATGACGCTCTGA - -AAAAGTGGAGATAATC 480
 Db 427 GAAATCCTCAGTGCACATCTCAGAAATATGATCCGAAATCGGAAATCTTATT 486
 Qy 481 TCGAGAGTGTGACGGCTGGCAGCAGGGTGATTCACCATGGAGAAATCTGGGT 540
 Db 487 GCAGAACCTTGGAAAGTGTGATTCAGAACGATCCATCTTGGAGAGCTAACGG 546
 Qy 541 ATGGAAACAGCTGAAAGTGTGAGGCTGCAATTGACGGCTGCAATTGACGGTGT 600
 Db 547 TCGAAACTGTTCTGAGGTTTACGAAATGACTTCACCGTGATCCCTCCAGC 606
 Qy 601 TACATGTCAGAGCAATGAAAGAAATGGTGTGAGACCTGTAACACCATTTATC 660
 Db 607 TACTTCCTCAGAACATCCAGAACATCTCAAGATGGTTTACAGAACGCTGATC 666
 Qy 661 ACGGATTAAGAAAGTCAACATCCAAAGCATTTCCACTACTTCTGGAGTCTAA 720
 Db 667 TAGGATTAAGAAACCTCGGAATTAAAGCTTCTCCAGTTTACACAGTGAGCA 726
 Qy 721 ACCACCGTCCATTACTATTTCTGAGTGTGAGTGTGAGCTCCACCTTCCACCT 780
 Db 727 TCTGAGCCCTCTTTATCATGTCAGACAGAAATGAGGAGAACCTTACACTA 785
 Qy 781 GCTCTGACAGAACATCGGCTACTTCATGGGGTCTCAAGGCGAGGATTGGT 840
 Db 787 GTAGTCATGACATCCCGAGCAGACTCTGGAGTCTGGAGAACCTCTGGTTGGT 845
 Qy 841 GATCGGCTGAAGATGATCTGAGCTGAGCACTGCTACTTCAGCTGTCAGTACA 900
 Db 847 GAGAGAGAGAGCTATGTTAGACATCGCTATCTACTGTTGGAGGTCTGAGCTA 905
 Qy 901 GAGGATCTAGCTGTTGATTAAGATGATCTCAATGACAGCCTTGACAGGGCTAG 960
 Db 907 GAGAACTTGGCTGAACTGAGATCAACTCTCAGTACGTTAGGAAAGCTAACGAA 966
 Qy 961 ATTACAGTTGAAAGATAGTAGGACACTAATGTTGAGGTTCTGAGCTGAGCTT 1020
 Db 967 GTTATCTGTAATGAGAATCACACATCGCGAGGTTAGAACACACTGATATC 1026
 Qy 1021 GCTAACCGTATTGACTGATTAATCGCAATTAGAACACAACTCTGACTTGTACCT 1080
 Db 1027 CAAAGCTGATGCGACAATTAAACAAATCGAGATAGCTACATCAGATTAGCAA 1086
 Qy 1081 GAAAATCTAACGACCTTGGCAATTAGTGTGGTACCTTCTCAAGGAGA 1140
 Db 1087 GAAAAACTTCCAGAGCGCTTAACTCACTCTCGGTTGQCCCTAAATCCGGTGA 1146
 Qy 1141 GCTCCACAGAGAGCTTAAAGAAATGAAACTCGATGAGGATCTCAATGCT 1200
 Db 1147 GCTGCTACCGHAAATGAGATGAGAAAGAACAGACAGTGATGATGATCACAGCA 1206
 Qy 1201 ACAGCTGACGCCGTTGAGAGGATCTCTGTTGGGAGACCACTTATAGGTT 1260
 Db 1207 ACCATTCAGCTGCTGAGGAGGATCTCCCTGGGGTGGACTCGCTTGTGGT 1266
 Qy 1261 ATGGAAAAACTTACAGCTCTGACTGCTGAG - - - - - GGGATGATCTGAGT 1311
 Db 1267 ATCCCTACACTAGAGTTCTCTCTGAGGAAAGCAGGAGCTATGGTACT 1326
 Qy 1312 ACATGTTGCTGTGCTGAGGAGCTGACTCAATGCTTAATGTTGGGTAC 1371
 Db 1327 CGTATTATCTAAAGCATACAGCTCTCAATTAGCAATGAGCTTA 1386
 Qy 1372 GAGGCTCCCTAATGAGCTGAAACACGCCCTGAGGAAAGCTTA 1311
 Db 1387 GAGGCTCTCTCTGAGGAGCTGAGGAGCTGAGCTGAGCTGAGCTGAGT 1446
 Qy 1432 GAGACAGGAGAGGGTGTGATGATTAACAGGAACTGACCTCTCAAGGACA 1491
 Db 1447 TTACGGTACGCTTATACAGATATGTTGACGAGGATTAGATCACAATGAGCT 1506

RESULT 6
 US-08-781-986A-266
 Sequence 266 Application US/08781986A
 Publication No. US20030054436A1
 GENERAL INFORMATION:
 APPLICANT: Charles Kunisch
 TITLE OF INVENTION: *Streptococcus aureus* Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5255
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
 COMPUTER: HP Vectra 886/73
 OPERATING SYSTEM: MS-DOS Version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A
 FILING DATE:
 REGISTRATION NUMBER: 30,445
 CLASSIFICATION: 435
 PRIORITY/DOCKET NUMBER: PB48PP
 REFERENCE/DOCKET NUMBER: PB48PP
 TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER:
 TELEPHONE: (301) 309-8504
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,445
 REFERENCE/DOCKET NUMBER: PB48PP
 TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER:
 TELEPHONE: (301) 309-8512
 INFORMATION FOR SEQ. ID NO: 266:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1017 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-781-986A-266

Query Match 29 5%; Score 483 6; DB 7; Length 1017;
 Best Local Similarity 67 2%; Preq No. 1.5e-108; Gaps 0;
 Matches 681; Conservative 2; Mismatches 331; Indels 0; Gaps 0;

Qy 1492 CGTCAGGCTCAAATGAGCTCTGACTACTTATTTGACACAGAGGAGT 1511
 Db 1507 CGCTCAGCTCTAGAAGCGCAGCTCTATCCGAGATTACTCTCCACACAGAACCTTA 1566
 Qy 1552 GTGCGTAACTGAACTGAA - -CCAGCTACGCCACGCCAGAACGCCA 1596
 Db 1567 ATGCCTGATTCAGAGAACATCTCTCAGTCCAGGATGCGCA 1614

Qy 1492 CGTCAGGCTCAAATGAGCTCTGACTACTTATTTGACACAGAGGAGT 1511
 Db 1507 CGCTCAGCTCTAGAAGCGCAGCTCTATCCGAGATTACTCTCCACACAGAACCTTA 1566
 Qy 1552 GTGCGTAACTGAA - -CCAGCTACGCCACGCCAGAACGCCA 1596
 Db 1567 ATGCCTGATTCAGAGAACATCTCTCAGTCCAGGATGCGCA 1614

Qy 1492 CGTCAGGCTCAAATGAGCTCTGACTACTTATTTGACACAGAGGAGT 1511
 Db 1507 CGCTCAGCTCTAGAAGCGCAGCTCTATCCGAGATTACTCTCCACACAGAACCTTA 1566
 Qy 1552 GTGCGTAACTGAA - -CCAGCTACGCCACGCCAGAACGCCA 1596
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RESULT 8

US 09-712-363-23

Sequence 23, Application US/09712363

Patent No. US2003016588A1

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TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

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 Db 901 GAAAGGGCTGGCTGAGAACGCGACCTCTCGCTGCTAACGGCGGAAG 960
 QY 961 ATTACAGTGTAAAGATGACGACAAATGTTGAGGTTCAGGAGTTGAGAGCTT 1020
 Db 961 GTCCTGGTCACCAAGGACGACACCCCTCGTGGAGGGCCGGCTGACACGGCTAC 1020
 QY 1021 GCTAACCTATTGACTGTTGATTAATGCAATTAGAACACAACTCTGACTTGTACCT 1080
 Db 1021 GCCGAGGAGGCGCAATCGCGGAGGATGGGAACGGACTTCAGGAGCTG 1080
 QY 1081 GAAAATCAGAGACGCTTAAGAAATGAAACTCGATGAGGATGCTTAATGCT 1140
 Db 1081 GAGAAGCTGAGACGCTGGGAAATTAGTGTGGGTTACCTGTTAACAGTGA 1140
 QY 1141 GCTCTAACAGAGACGCTTAAGAAATGAAACTCGATGAGGATGCTTAATGCT 1200
 Db 1141 GCGGCACCGGGTGGTGAACGAGGACGACCCATCAGGAGCTGAGGTTGCAAT 1200
 QY 1201 ACAGCTGCAAGGCTGAGAAGGATGCTGGTGTGGGGGAAACACACTTAACTGGT 1260
 Db 1201 GCCAGGGCGCGTGGAGGGCGATCGTCGGCGGGGGTGAGCTGTTGCAAGG 1260
 QY 1261 ATTGAAGAAATGAGCTGCTGTTGAGTTGGGGCGTGTACTGAGCTAACATG 1320
 Db 1261 GCGCCGACCCGGAGACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
 QY 1321 CTGGTGTCTAAGAACCTGTAGCTAAATGCTTAATGCTGGTACGGCTC 1380
 Db 1321 AASGTGGCGCTGGGGCCCTGGAGGAGATGCTCTCACTCCGGGGAGCGGG 1380
 QY 1381 GATGTTATGACAGACTGAAACACCCCTGGAGGACAGATTATGCTGAAGG 1440
 Db 1381 GTGGGGCCGAGAAGGTCGACCTGGGGCTGACGCTCAGACGGT 1440
 QY 1441 GATCTGGTTGATATGATTAACAGAACGAAATCATGGCCCTGTCAGGATACCGATAGGG 1500
 Db 1441 GTCAGCAGGTCCTGGCTGGCTGGCGCTGGTGGCCCTGGTGGCG 1500
 QY 1501 CTCTAAATGCACTCTGAGTCTGTTGAGCTCTTATGACACAGACAGTTGTGTTAAT 1560
 Db 1501 CTCTGAGATGCGGGTCCATGGGGCTGTCGACCGGCCCTGTCGGAC 1560
 QY 1561 AACCTGAA 1569
 Db 1561 AASCGGAA 1569

RESULT 9
 US-10-267-311-3
 ; Sequence 3, Application US/10267311
 ; GENERAL INFORMATION:
 ; APPLICANT: Siegel, Marvin
 ; APPLICANT: Chu, N. Randall
 ; APPLICANT: Mizzen, Lee A.
 ; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
 ; FILE REFERENCE: 12071/002001
 ; CURRENT APPLICATION NUMBER: US10-267-311
 ; CURRENT FILING DATE: 2002-10-09
 ; PRIORITY NUMBER: US09/613,303
 ; PRIORITY FILING DATE: 2000-07-10
 ; PRIORITY APPLICATION NUMBER: US 60/143,757

PRIMER FILING DATE: 1999-07-08
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 1623
 TYPE: DNA
 ORGANISM: Artificial sequence
 FEATURE: OTHER INFORMATION: fusion sequence
 FEATURE: NAME/KEY: CDS
 LOCATION: (1)...(1620)
 US-10-267-311-3

Query Match 28.0%; Score 458 6; DB 9; Length 1623;
 Best Local Similarity 55.8%; Pred. No. 2,66-112; Matches 875; Conservative 0; Mismatches 634; Indels 0; Gaps 0;
 Db 1 ATGGCAAAAGAATCATTTCAGGAGATGGCTGTCGCGGAGGTGT 60
 Db 61 GCCCTCGGGATCGGTAAGGGTACATGGCCCGAACGGCGCTCGACGGGCTGAC 60
 Qy 61 ATGGCAAAAGAATCATTTCAGGAGATGGCTGTCGCGGAGGTGT 60
 Db 181 CTGGAGGATGCTGAGGAGATGCTCTCAACGGCGCTGAGAG 240
 Qy 121 AAAGCTTGTGCTCCCTTAATCTAACTAATGACGGGTAACATGCTAAGAGTGA 180
 Db 121 AAGAATGGTGGCCCGACGATCACAAGAAGGTTGTCATGCCAGGAGATCGK 180
 Qy 181 TTAGAGATCTTGTAAACATGGGCAAAATGGGTGTTGAGTGTCTAAAC 240
 Db 301 GAGGACTAAATGTCACGGAGATGCGGCGGAGCTGTCGAGAG 240
 Qy 241 ATGATTTGCGTGGATGGAGATCTGGCAGCTGACAGTTGGACACAGCTTGTCTAC 300
 Db 241 GATGAGCTGGCGGTGACCGCACAGGACGGCCACCTCTGGGCCAGGGTGTGG 300
 Qy 301 GAGGACTAAATGTCACGGAGATGCGGCGGAGCTGTCGAGAG 360
 Db 301 GAGGCGCTCGAACCTCCGGCGGCGCAACCGCGCTGCTCTCACAGGGCTAC 360
 Qy 361 ACAGCAACGACACAGCTGAGCTGTCGAAAGCTTGTCTCACCTGTATCGCAAG 420
 Db 361 AAGGGCTGGAGAGTCACCGAGGCTCTCAGGGGCCAGGGTGTGGAC 420
 Qy 421 GAGGATATGCTGAGGTCTGGCTGGAGTATCATCACGCTGTCGAAAGTGGAGGATATC 480
 Db 421 GAGCAGATGCGGCCACCCGACGGATTCGGCGGGACCTGTCGTC 480
 Qy 481 TCAGAGCTATGGAGGCTGGCAACGATGGTGTGTTACATGAGAATCTGGGT 540
 Db 481 GCGGAGGATGACAGGGGGCAACGGGGTCTCACCGTGAGGACTCCAC 540
 Qy 541 ATGAAACAGAACTGCACTGCTGTGAGGACGATGCAATTGGCTGGTACCTGCTCA 600
 Db 541 TTGGGCTCAGCTGGAGGATGGGTGACGGCTACATCGGGG 600
 Qy 601 TACAGGGTACAGACAGATCAAATGGTGTGAGCTGACGCTTGTGAAACCTTATCTAATC 660
 Db 601 TACTCTGGTACGGACCCGGAGCTCAGGGCGCTCTGGGGACCTCTAGATCTGCTG 660
 Qy 661 ACGGATAAAAGTGTCAACATCAGACATTTGCACTACTGTGAGAATGTTAA 720
 Db 661 GTCTGTCACAGTGTCTCCACTGTCAGGATCTGCTGCGGCTGCTGAGGTCTCGGA 720
 Qy 721 ACCAACGCTCATCTACTCTATGCAAGGAGTGTGAGGACTTCACCCCT 780
 Db 721 GCGGTGAGGCTGTCATCGCGAGGAGTGTGAGGAGGGCTCTCCACCTG 780
 Qy 781 GCTCTGACAGACAGATGGTGTGTTCTCAATGTGTTCTGTGCAAAAGGCCAGGAATTGGT 840
 Db 781 GTCTGACAGACAGATGGTGTGTTCTCAATGTGTTCTGTGCAAAAGGCCAGGAATTGGT 840

US-10-267-311-20

Query Match 28.0%; Score 458.6%; DB: 9; Length 2847; Best Local Similarity 55.8%; Pred. No. 3; 3e-102; Matches 875; Conservative 0; Mismatches 694; Indels 0; Gaps 0

QY 961 ATTACGTTGATAAAGATGATGCAAGTATGTTGAAAGTTCAGAACCTATT 1020

Db 1285 GTCCTGTCACCAAGACGACCACTCGTGGAGGCGCCGTCAGCACCCATC 1344

QY 1021 GCTAACCTATGCACTGTATTAAATGCAATTAGAACACAACTTCAGACTG 1080

Db 1345 GCGCGACGAGTGGCCAGATCGCCAGAGATGAGACAGCGACTCGACTAC 1404

QY 1081 GAAAACCTACAGAAGACGTTGCGAANATTGCGCTGGTGTAGTGTATCAAGTAGGA 1140

Db 1405 GAGAGCTGCAAGGAGGGCTGCAACGACGCTGCGGCTGCGGGATGAGA 1464

QY 1141 GCTCCAAAGAGACGCTTTAAAGAAATGAACTGCACTGGGATGCTTAATGCT 1200

Db 1465 GCGCGACGAGTGGTGAACCTCAAGGAGCGACACCGCATGGGGATGCGCAT 1524

QY 1201 AACAGTGCAGCGGTGAAGAAGTGTGAGTGTGCGGTGAGACAGACTTATGCTT 1260

Db 1525 GCGAGGGCGCGTCAGGAGGGCATCTGTCGCGGGTGGGGTGGACTG 1584

QY 1261 ATTGAAAGAAAGPRAGCAGCTTGTAGCTGGGGATGATGCTACTGGACGTAATGCT 1320

Db 1585 GCGCCGACCCCGTGGACGAGCTGAGCCTCGAGGGGACGGGGCCAACTCTG 1644

QY 1321 CTGGTGTCTAGAAGAGCCTTACCTCAATGCTTTAATGTTGGTACAGGCTCC 1380

Db 1645 AAGGTGGCGGGGCGCTGAGCGATGCGCTTCACCTGGGCTGAGCCGGC 1704

QY 1381 GTAGTATGCAACTGAAACACCCCTGAGGACAGATTAAATGCTGACACAGT 1440

Db 1705 GTGGTGGCGGAGGAGTCGCGACCTGGGGCTGGCACGAGCTGACGCGT 1764

QY 1441 GACGGGTTGATGATTAACAGACGACATGACCCCTCAAGAACGGATTCGG 1500

Db 1765 GTCTACAGGAGCTCTGCTCCCGCGTGGAGCCGGTCAGGGTACCCGGT 1824

QY 1501 CTCAAATGAGCTGCTGCTACTGTCTTATTTGACACAGACGAGCTGCTAT 1560

Db 1825 CTGGAGATGGGCCCTACCCGGGGTGTCTCACCCAGGCGTCGCGAC 1884

QY 1561 AACCTGAA 1569

Db 1885 AAGCGGAA 1893

RESULT 12

US-10-267-311-20

; Sequence 20; Application US/10267311

; Publication No. US2003050469A1

; GENERAL INFORMATION:

; APPLICANT: Siegel, Marvin

; APPLICANT: Chu, N. Randall

; APPLICANT: Mazzoni, Lee A.

TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO

FILE REFERENCE: 1120714/002001

CURRENT APPLICATION NUMBER: US/10/267, 311

PRIOR APPLICATION NUMBER: US2002-10-09

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143, 757

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO: 20 LENGTH: 2847

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: fusion sequence

FEATURE: NAME/KEY: CDS

LOCATION: (1... (2844)

QY 1 ATGCAAAAGAAATCAATTTCAGACATGCGCTACGACCGT 60

Db 61 ATGGCAGACGACATGCTGAGACGAGAGGGCCGTCGGGCTCAGGGGGCTGAC 120

QY 61 ATGTTACAGATACGCTGAAGTAACTGCTGTTGCTCTAAAGGGCAATGTTCTGAA 120

Db 121 GCCTCCCGATGGGTTAAAGTGTGACATGGCCCAACGGGCCACGCTGCTCGGA 180

QY 121 AAAGCTTGTCTCTTAACTATGACGGGTTACCATGCTAAAGATGCAA 180

Db 181 AACAGCGGGCCACGATCACACAGCTGAGTGTGTCATGCCAAGGAGTCAG 240

QY 181 TTGAGATATTGAAAGATGGACGACATGGGACAAATGTTCTGAGTGTCTAAAC 240

Db 241 CTGGAGATCGTAGGAGATGGCCCTGAGCCTGAAAGAGTACCAAGAAC 300

QY 241 ATGATTTGCTGTTGGGAGACTCTGCAACAGTTGACACAGCATGTT 300

Db 301 GATGACCTCCCGTGGAGGACACGAGCGACGGCTGCGCAGGGTGGATCG 360

QY 301 GAGGATTAATGACGACGACGACGACATGGTCTGAGTGTCTGAGGCTGA 360

Db 361 GAGGGCTGGCGCACAGCTGGCGGCGGCCAACCGCGTGGCTAACCGCGCATCGAA 420

QY 361 ACACGACACGACGACGACGACGACATGGTCTGAGTGTCTGAGGCTGA 420

Db 421 AAGCCGTTGAGGAGGGTACCGACCTGTCTGAAACGCTTCACTCTATCTGCGA 480

QY 421 GAGCTTCTCTGGTCTGAGTATCATCACCTCTGAAAGATGGAGATATC 480

Db 481 GACGACATTCGGCACCGACGCGGCAATTGGGGTGTACAGTCCTGGTACCGTAC 540

QY 481 TCGAAGCTTGGGGCTGTGGGACACATGTGTGATACATGGATGAGAATCTGAGG 540

Db 541 GCGGAGCGGTGACGGGGTACCGACGACCTGTCTGAGGGCAAGAGGCTCGAC 600

QY 541 ATGGAAACAGACACTGAGTGTGTTGAAGGCTGATTTGACCGTGTAACTGTCTCA 600

Db 601 TTGGCTGAGTCGAGTCACCGAGGGTGGGGTGGAGGCTACATCTGGG 660

QY 601 TCTAGTCTCACAGATGAAATGGAGACGACTGAGACCTTATTCATTC 660

Db 661 TACTTGCTGACCCGCGGAGCTGGGGCTCTGGAGGACCCCTACATCTCTG 720

QY 661 ACGGAAAAAGTGTCAACCTCAGGACATTGGCACTTGAGGAGTCTTAA 720

Db 721 GTGAGCTCCAGGGTGACCTGCTGAGATCTGCTGCTGCTGAGATCTGCA 780

QY 721 ACCAACCGTCATTACPCATTGAGATGATGGATGGTGAAGACCTTCACCCCT 780

Db 781 GCGGGTAAGCGCGTGTGATCATGCCGGAGACGCTGCGAGGGCGCTGTCACCG 840

QY 781 GCTTGTACAGATCTGTGACTCTCAATGTTGTTGCTGAAGACGCGCAGATTGT 840

Db 841 GTCGTCACAGATCTCCGGCACCTTCAGTGGTGGCTCAGCTCCCGCTCGC 900

QY 841 GATCGCTGTAACCTAGTGTGAGGATCTCTCTGAGGGTGTACCTGTATA 900

Db 901 GACCGCGCAAGCGATGTCGAGGATATGGCTTCACGGGGTGGCTGATCAG 960

QY 901 GAGGAGTCAAGTGTGATTAACAGATGCTACAGACAGCCTGGAGACGCTCTA 960

Db 961 GAGAGAGTGGCTGAGGAGACGGGACCTGTCGTCGTCAGGAGCGCAG 1020

QY 961 ATTACGTTGATAAAGATGAGCTGATTTGAGGTTAGGAGTTCAGAAGTATT 1020

Db 1021 GTCGTCACAGATCTCCGGCACCTTCAGTGGTGGCTCAGCTCCCGCTCGC 1080

us-09-738-626-2986

Query Match 27.9%; Score 457; DB 9; Length 1644;
 Best Local Similarity 56.4%; Pred. No. 6.4e-102; Matches 903; Conservative 0; Mismatches 680; Indels 18; Gaps 2; Matches 903; Conservative 0; Mismatches 680; Indels 18; Gaps 2;

Qy 1021 GCTAACGGTATTCAGTAACTAACCAATTAAACACAACTTCGACUTTGACCGT 1080
 Db 1081 GCGCGACGAGTAGGCCAGATGCCAGAGACAGACAGACGACTTCGATAGCCG 1140
 Qy 1081 GAAACTACAGAAGCTTGGGAATTAGCTGTGTGTGAGTTAACTAGA 1140
 Db 1141 GAGAACGTCAGGGCTGAGGCTGAGGAGCTGGCTGAGTCAGCGCGT 1200
 Qy 1141 GCTTCAACAGAGAACGACTTAAAGAATGAACTTCGATGAGATGCTAAATGCT 1200
 Db 1201 GCGCGACCGAGCTGACTCACAGGAAAGCAGCAGTCAGGAGTCAG 1260
 Qy 1201 ACACCTTGAGCGCTGAGAAGTAACTGTGTGTGAGTGAAGAGCTATTACGTT 1260
 Db 1261 GCGAAGGCGCCTCGAGGGACATGTGCGGGTGTGAGCTGAAAGC 1320
 Qy 1261 ATGAAAGATGTCACCTCTGAGCTGAGGGATATGCTACTTGACATG 1320
 Db 1321 GCGCGACCTTGAGGAGTGAAGCTGAGGAGTCGGAGGAGGGCACCG 1380
 Qy 1321 CTCTGCTCTAGAAGAGCTGAGCTGACATTCGTTAAATGTTGCTGAGGCTC 1380
 Db 1381 AAGGGGGGCTGAGGCCCGCTGAGGAGTCGCCCTCACTCGGCGTGGAG 1440
 Qy 1381 GTAGTATGCAAGTGTGAGCTGAGGAGTATGCTACTTGACATG 1440
 Db 1441 GGGGGGCGACAGATGGCCGACCTTGCGCGGAGCAGCTGACACCGT 1500
 Qy 1441 GAGGGGCTGATGTTAAACAGGAACTACGACGCTGCAAGAACGATCGCG 1500
 Db 1501 GCTCTACGAGGAGTCGTCGTCGCGGGTGTGAGCCCGTCAAGGTCGGCG 1560
 Qy 1501 GTCACAAATGCGCTCTGAGCTAGTCTTATTTGACACAGAGCAGTGTGCTAT 1560
 Db 1561 CTGCKAGAATGCCGCTCCATCGGGGGCTTCTCTGACCCACCGAGGCGCTG 1620
 Qy 1561 AACCTGAA 1569
 Db 1621 AACGGCAA 1629

RESULT 13
 US-09-738-626-2986
 ; Sequence 2986, Application US/09738626
 ; Publication No. US2002196051
 ; GENERAL INFORMATION
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIJI
 ; APPLICANT: HAYASHI, MIKRO
 ; APPLICANT: Ochiai, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAKO
 ; APPLICANT: SEMOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIORITY APPLICATION NUMBER: JP 99/377484
 ; PRIORITY FILING DATE: 1999-12-16
 ; PRIORITY APPLICATION NUMBER: JP 00/159162
 ; PRIORITY FILING DATE: 2000-04-07
 ; PRIORITY APPLICATION NUMBER: JP 00/280988
 ; PRIORITY FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 709
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO: 2986
 ; LENGTH: 1644
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum

Qy 1 ATGGCAAAAGAACAAATTTCAGCAGATGGCGGCGCCATGTCGGAGTG 60
 Db 1 ATGGCAAAAGAACAAATTTCAGCAGATGGCGGCGCCATGTCGGAGTG 60
 Qy 61 ATGTTACAGATACCGTCAGTAACTGACGCTGTCCTTAAGGGCGCATGTCGAT 120
 Db 61 ACCCTGCGTCAGCGTGTAAAGTACTTGGACCAAGAACGGCTACGTCG 120
 Qy 121 AAAGCTTGTGTTCTTAATCTACTATGAGGGTAACTTCTAAAGATGCAA 180
 Db 121 AAGCTTGTGGCTGGCCACCCATTACACAGATGTTGTCACCTCCACGATGAG 180
 Qy 181 TTAGAGATCAATTGAAAGATGGGAGCAATGGGGCAAAATGGTGTCTGAAGTGGCTTAANACC 240
 Db 181 CTGAGGATCTTACGAGGAGTGGCCGAGCTGTCGAGTCAGTCGTTAGAGACT 240
 Qy 241 ATGATATTCGTTGATGGAGGACTACTGACAGCTTGTACAGAACGCTTGTCA 300
 Db 241 GATGACCTCGGGCGGAGGACCAACCCSCTACCGTATGGCACAGGCTCTGGTCGG 300
 Qy 301 GAAGGACTAAATGAGCAGCGGGTCTATCCAAATGCTGATCGTGTGAGCTGAA 360
 Db 301 GRAGGCTGGCGACAGTGTGCTGCTGCTTACCCAAATGGCATCGCGATCG 360
 Qy 361 ACAGCACACACAGCTGTTGAGGCTTAAAGACATGTCACCTGTATGGCAAG 420
 Db 361 AAGCTTGTCTCGGPACTGAGAAGCTGTCGAGGCTGGAGGAATGGACCGAG 420
 Qy 421 GRAGCTTACTGAGGCTGTGGG-----GAGCTGAAAGTGGAGGTATC 480
 Db 421 GAGCAATCTCTGCTACGGCGPATCCTCCAGCTGACCTGACCGAGTCCCTACGATT 480
 Qy 481 GCTAACGGTATTCAGTAACTAACCAATTAAACACAACTTCGACUTTGACCGT 540
 Db 481 GAGAACGTCAGGGCTGAGGAGCTGGCTGAGTGAAGAGCTGGCTGAG 540
 Qy 526 GAGAACTCTGAGGTATGGAACAGACTGAGCTGGTGTGGATGAAATTGACCGT 595
 Db 541 GAGAGGCCACACTTGGGTTGAGCTCGAGGTACTCTGAGGTGTGGCTTGTGATAAG 600
 Qy 586 GGTACTCTGCTCAATGAGGAGCAGACATGAAAGGGTGTGAGCAGCTGAAAC 645
 Db 601 GGTCACATCCGGTTACTTCGCACTTCGCACTTCGAGGCGCCCTGGAGAT 660
 Qy 646 CCATTCTACATCAAGGATAAAAGTGTCAACATCAGACATTTGGCAGACTT 705
 Db 661 CCTTACATCTGGTTTCGGCAAGATCCTCCACACATCAGGAGCTGTCACGCTG 720
 Qy 706 GAGGAGCTTAAACCAACGGCTATTCATTTAGCTGAGATGTGATGTGAA 765
 Db 721 GAGAAGTCTGAGGCCGCAAGCTTGTGTCATCTTGAGGAGCTGGCG 780
 Qy 766 GCACTCCACCTGTCTGAGCAGTGTGGTGTGACTTAAAGATGGTACATGTCGACGCC 825
 Db 781 GCTCTTCCACCTGGTGTGAGCAACACATCTGGTGTGTCGACGCC 840
 Qy 826 GCGCAGGATTTGCTGATCTGAAAGCTGATGAGCATGTCGTCGACGGT 885
 Db 841 GCTCCGGCTTCGGCAGCTGCTGAGCTGCTGAGCATGTCGTCGACGGT 900
 Qy 886 GGTACAGTATCACAGGTCAGGACTGAGTAACTGAGTGTGACATGTCGACGCC 945
 Db 901 GCGCAGGATTTGCTGAGGAGTGGCTCTCCCTGAGCGCGTACGTCGACCTC 960
 Qy 946 GGACAGCTGCTAGATGAGTGTGAGCAGACGATATGGTGAAGTGTGAG 1005
 Db 961 GCGCAGGACGAGGTGTGTCACCAAGATGACACACATCTGGTGAAGGCC 1020

US-09-738-626-1	
Query Match	27.9%; Score 457; DB 9; Length 3309400;
Best Local Similarity	56.4%; P: 0.3-4e-100; Mismatches: 903; Indels: 18; Gaps: 2;
Matches	903; Conservatism: 56.4%; P: 0.3-4e-100; Mismatches: 903; Indels: 18; Gaps: 2;
QY	1066 AGTCAGAGCTTACCTTACCGCTTACGACTTAAATGCAATAGAACACAACT 1065
Db	TCTGAGGCTCTGACATGAGCGCGTCAACAGACATCGCTTGAGATCGACCT 1080
QY	1081 TCCCACTGACCGTGAGAGCTCACAGCGCTGAGCTTAAGCTTGGCTACT 1125
Db	1121 GTTATCACAAAGTGGAGCTCACAGAGACGCTTAAGAAAGTAAACTCCGAT 1140
QY	1126 GTTATCACAAAGTGGAGCTCACAGAGACGCTTAAGAAAGTAAACTCCGAT 1185
Db	1141 GTGTTAAAGGGGGCGACCTACCGGGTGTGACCTAAGGGCGACCGCTG 1200
QY	1186 GATGCTCTAAATGCTACAGTCACGGCTAGCGGTGAGAAGGATCCGCTTAC 1245
Db	1201 GATGCTCTCCAACTGCTAACGCTAACGCTGTGAGAGGGCTTGGCGGGGG 1260
QY	1246 GCATTTAGGGTATGAAAGTAG--GAGCTTGAGCTGGGGGATGATCT 1302
Db	1261 GCGCTGCGCAGGCGCTACCTCCGGCAAGGATCTGAGCTTCCGGCGAGGCA 1320
QY	1303 ACTGAGGCTAACATGCTGGCTGCTGAGAGGCGCTTACGCTTAAAT 1362
Db	1321 ACGGGCTTCCGCTGCGGGAGGCTGACTGCTCTGAGCAGATGCTGCA 1380
QY	1363 GCTGGGTACGAGGAGCTCGTAGTTTGTGAAACGCGCTGAGCTGAGGAGCA 1422
Db	1381 GCTGGCTCTGAGCCAGGGTGTGCTGCAAGGTTCTCCACGGGGAGGG 1440
QY	1423 TTAATGCTGCAACAGGTGAGGGTTGATATGATAAACAGGAACTGACCTG 1482
Db	1441 CTCACAGCTGCAACGCGAGTCTGACCTCAGCTGCGGGCATCACGACCTG 1500
QY	1483 AAGTAGAACAGGATGAGGCTTAAATGAGCTCTGACTGCTTATTTGAAACA 1542
Db	1501 AAGTCACCCGCTCGACTCGAGCTGCTGATCATGAGCTGTGCTGAGCACT 1560
QY	1543 GAAGCAGTTGTTGCTTAATACCTGAGAACGAGCTAGGCCAGC 1583
Db	1561 GAAGCAGTTGTTGCTTAATACCTGAGAACGAGCTAGGCCAGC 1601
RESULT 14	
US-09-738-626-1/C	
Sequence	1. Application US/09738626
Publication No.	US20020197605A1
GENERAL INFORMATION:	
APPLICANT:	NAKAGAWA, SATOSHI
APPLICANT:	MIZOGUCHI, HIROSHI
APPLICANT:	ANDO, SEIJI
APPLICANT:	HAKASHI, MIKIRO
APPLICANT:	OCHIAI, KEIKO
APPLICANT:	YOKOI, HARUKO
APPLICANT:	TATEISHI, NAROKO
APPLICANT:	SENOH, AKIHIRO
APPLICANT:	IKEDA, MASATO
APPLICANT:	OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES	
FILE REFERENCE: 249-125	
CURRENT APPLICATION NUMBER: US/09-738-626	
CURRENT FILING DATE: 2000-12-18	
PRIOR APPLICATION NUMBER:	JP 99/377484
PRIOR FILING DATE:	1993-12-16
PRIOR APPLICATION NUMBER:	JP 00/159162
PRIOR FILING DATE:	2000-04-07
PRIOR APPLICATION NUMBER:	JP 00/280988
PRIOR FILING DATE:	2000-08-03
NUMBER OF SEQ ID NBS:	7059
SOFTWARE:	Patentin ver. 3.0
SEQ ID NO:	1
LENGTH:	3309400
TYPE:	DNA
ORGANISM:	Corynebacterium glutamicum

QY 1005 ACTTCAGAAGCTTCTAACCCCTTTGCACTTTAAATGCCATTAGAACACACT 1065
Db 2889520 TCTGAGGTCTGAGTCGAGGCGGCGTCAACCGAGATCGGGTGAGTCGAAGCTCGAT 2889451
QY 1006 TCTGACTTGTGACCGTGAACACACAGAACGCTTGGCAAAATTTAGATGGGGTGCT 1125
Db 2889460 TCCGACTTACGACCCGTTGAGAACGCTCACAGCGCTGCTGAGCTTGAGCT 2889401
QY 1126 GTTATCAAAAGTAGGAGCTCCACAGAGACAGCTTAAAGAACATGAACTTCGATG 1185
Db 2889400 GTCTCTTAAAGGGGGCGCGAGCTTACCCAGGGTGTGAGCTCAAGGAGGCGAC 2889411
QY 1186 GATGCTCTAAATGCTACAGTGCGAGCGGTGAGAAAGTATCGTGTGAG 1245
Db 2889340 GATCTCTCCGTTAACGGCTAACGGCTAACGGAGCTGTTGAGAGGGATGTTCCCGCGT 2889281
QY 1246 GCTATTTAATAGCTTATGAAAGTAG -- CAGCTCTGAGCTTGAGGGATGATCT 1302
Db 2889280 GCGCTGCTGAGGTGCTCACGCTCTGGACACAGCTTGGCTTCCCGACAGGGCA 2889221
QY 1303 ACTGGACGCTAACATGCTGCTGCTGAGAGCTAACGGCTAACGGCTTAAAT 1362
Db 2889220 ACCGGCTTTCGACGCTGCTGGAGGCTGACTGCTCCCTCTAACAGAGCTG 2889161
QY 1363 GCTGGGTGAGGCTCGTGTGAGTATTTGAGCTGAGTGAACACGCTGAGCTTCC 1422
Db 2889160 GCGGGCTCTGAGCAGGGCTGTTGCTGAGCAAGGTTCCACAGGGGGGG 2889101
QY 1423 TTATGCTGACAGGTTGAGTGGTTGATGATAAACAGAACTATGACCTGCTGCTG 1482
Db 2889100 CTCAAGCTGCAACAGCGAGTGTGGCTCTGGTGGGGCATCACACCCAGT 2889041
QY 1483 AAGTAACACGCTGAGGCTTCATATGAGCTTGTGAGCTAGTTATTGACCA 1542
Db 2889040 AAGTGTACCGCTGGGACTCAGCAAGGCTCACCATGAGCTCTGTCTGACACT 2889191
QY 1543 GAAAGCTGTGTTAAACCTGAAACCGCTAGGCCAG 1583
Db 2889890 GAGGCTGCTCTGCTGACAGCACGCTGAGGCCAGCGCAGC 288940

RESULT 15

US-10-068-059-9
; Sequence 3, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 1201-017002
; CURRENT APPLICATION NUMBER: US/10-068-059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NO: 12
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein

Query Match 27.8%; Score 455 6; DB 9; Length 2073;
Best Local Similarity 55.7%; Pred. No. 1.5e-101;
Matches 872; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

QY 4 GCAAAAGAAATCAATTTCAGGAGTGGCGGCTGCCATGGGCCGAGTGTATG 63

Db 454 GCAAGAACATTGGTAGAGCAGGAGCGCCCGCCCTGAGGGCTTGAGGCC 513
QY 64 TTACACAGTACCGTCAGAAACACGCTTGGCTTAAGGGCAATGTTGTCGAGAAA 123
Db 514 CTGGCATGGTAAAGGGCACATGGGCGCAAGGGCGCTGAGCTCTCGTGGAAA 573
QY 124 GCTTTGTTCTCTTAAATCTAACATGACGGGAAACCTGAGCTAACAGCTG 183
Db 574 AKTGGGGTGCCTCCAGGATCACGACGATGGTGTGTCATGCCAGGATGAGCTG 633
QY 184 GAAAGCTATTTGAAACATGGGCAAAATGGGTGAGTGTGAGTGTGCT 243
Db 634 GAGGACGCTTACAGAGAGTGGGGGAGCTGGTCAAGAGGTGACCGGAT 633
Db 754 GGCTGGCGCACGTCGGCGCGGCGAACCGCGTCGTCGACAGGGCTGGAANG 813
QY 364 GAAACAGCACACGCTTGTGAGCTGAGCCATGTCACCTGATCTGCGAGGA 423
Db 814 GCGTGGAGAGTCAACGGACATCTTACGGCGCAGGAGGTGGAGCCAGGG 873
QY 424 GTATATGCTGAGCTGCTGAGTATCAGCTGGCTGAAAGTGGAGTATCAG 483
Db 874 CAGATGCGCCACCGCCAGSGATTTGGCGGGTGGACGTCTGGTACCTGGCGCC 933
QY 484 GAGCTATGAGGTTGGCGAACGAGTGGGGTGTACACGAGAACTCGAGGTG 543
Db 934 GAGGGATGGACAGSTGSGCANCAGGGGTCATCCCGTGGAGTCCTAACCTT 993
QY 594 GAAAGCTGAGCTGTTGAGGACATCAATTGCGCTGAAACCAATTATTCAGG 603
Db 994 GCGCTGCGCTGAGCTGGCTCCCGAGGTATCGGTTGCTGACAGGGCTACATCGGGTAC 1053
QY 604 ATGGCAGACGAACTGAAATGGTGCAGCTGAAACCAATTATTCAGG 663
Db 1054 TTCTGACGCGACCCGGAGGTCAAGGGGGCTCTGGAGGGCCCTACATCTGGTC 1113
QY 664 GATAAAAGCTGACACTCCAGACATTTGCCACTACTTGGAGGTCTTAACCC 723
Db 1114 AGCTCCAGGTGTCCTACTGTCAAGGATCTGCTCGCGTCTGAGGTCTCGAGCC 1173
QY 724 AACGGCTCAATRACTATTTACGGATGATGGATGGGATGAGCACTCCACCTGTC 783
Db 1174 GGTAGCCGCTCTCTTCAGCCGGAGGGTGGAGGGCGCTGTCACCTGGTC 1233
QY 784 TTGACAGAGATGCGTGTCTCTCATGGTGTGCGTCAACGGCAGATTTGGAT 843
Db 1234 GTCACAGACGTCGGGGACCTCTGAGCTGAGCTGGCGTCAAGGCTCCGGCTGGGAC 1293
QY 844 CGTGTAMAGTATCTGAGACAGTGTCTGAGCTGAGCTGAGTACAGTGACAGG 903
Db 1294 CGCCGCGAGGCGAGTGTGGAGTATGCGCATCTCACGGTGTGAGCTAGCGA 1353
QY 904 GATCTGAGCTGATTAAGAGTGTACATGACGCGCTTGACAGGGCTGTAACATT 963
Db 1354 GAGGTGGCCGAGCCTGAGACGCCGCGCTGCTGCTGAGCAGGGCCAGGTC 1413
QY 964 ACAGTTGATAGAGTACGAGTATGTTGGAGTTGAGGTGAGAGTGTATGCT 1023
Db 1414 GTGGTACAGGAGGACACCTCGTGGAGGCGCGCTGACACCGAGCTGAG 1473
QY 1024 AACGGTTGCTGAGCTGATTAAGTCAATGACACACTCTACTTGACCGGAA 1033
Db 1474 GGAGGAGTGGCCAGACCTCGTGGAGGCGCGCTGACACCGAGCTGAG 1533
QY 1084 AACTACAGACGCTTGGCAAAATTACTTGGTGTGAGCTGTTATCAAGAGGGCT 1143

Db 1534 AAGCTGCAGGGGGCTGGCAAGCTGGCCGGTGTGGCGGTGATCAAGGCCGGTGC 1593
 Qy 1144 CTCACAGAGCACTTAAAGAATGAACTTCCATGAGCTCTTAATGTTACA 1203
 Db 1594 GCCACCGAGTCGCACTCAAGGAGGCAAGGCCATCGAGTCGGTCCAAAGGCC 1653
 Qy 1204 CCGCGACCCPTGAGAGGTTATGGTGTCTGGTGTGAGCAGCTTATAGGGTT 1263
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 Qy 1264 GAAAGTAGCAGCTCTGAGCTGAGGCGATGAGTACAGTGGAGTACATGCTT 1323
 Db 1714 CGGACCTGGACAGCTGAAGCTGAGCTGAGGCGACGGGCCACATCGTGAAG 1773
 Qy 1324 CCTGCCTCTGAAAGCTGAGCTGAGCTGAGGCGACGGGCCACATCGTGAAG 1773
 Db 1774 GTCGCCTGGAGGCCGCGTGAACAGATCGCTCACTCGGGCTGGAGCGGGCGT 1833
 Qy 1384 GTTATGACAGTTGAAACAGCCCTCAGGACAGGATTAATGCTGAGTCAACAGGTAG 1443
 Db 1834 GGCGCGAGGGTGCACACTGCCGGCTGGCCGGACTGAGCTCAGCCGGTGC 1893
 Qy 1444 TGGTGTATGTTAAACAGGATATTCACCTGTCAGATACAGTACAGGCTT 1503
 Db 1894 TACGAGACCTGTCGCGGGGTGACCCGGTCAAGTGGCCGGTGGGGCTG 1953
 Qy 1504 CAAATGCACTCTGAGCTAGTCTTGTACAGAGCAGTGTCTTGTAA 1563
 Db 1954 CAGAATGCGCGTCATCGGGCGCTGTTCTGACACCGAGCGTGTGCGACAG 1953
 Qy 1564 CCTGAA 1569
 Db 2014 CGGGAA 2019

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